

SEQUENCE LISTING

<110> Albone, Earl F.
Soltis, Daniel A.

<120> ANTIBODIES THAT BIND CELL-ASSOCIATED
CA 125/O772P AND METHODS OF USE THEREOF

<130> 6750-214-999

<140> To be assigned

<141> 2003-10-15

<150> 60/485,986

<151> 2003-07-10

<150> 60/418,828

<151> 2003-10-12

<160> 71

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 748

<212> PRT

<213> Artificial Sequence

<220>

<223> CA 125/O772P 3-repeat

<400> 1

Ala	Ala	Gln	Pro	Ala	Arg	Arg	Ala	Arg	Arg	Thr	Lys	Leu	Phe	Thr	His
1				5				10						15	
Arg	Ser	Ser	Val	Ser	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	Tyr
			20				25					30			
Leu	Gly	Ala	Ser	Lys	Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	Ala
		35				40					45				
Ser	His	Leu	Leu	Ile	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu
	50				55			60							
Arg	Tyr	Glu	Glu	Asn	Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
65				70				75						80	
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser
			85				90						95		
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu
		100					105						110		
Lys	Asp	Gly	Glu	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro
	115					120					125				
Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu
	130					135					140				
Ser	Gln	Leu	Thr	His	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp
145				150				155						160	
Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Pro
			165				170						175		
Thr	Thr	Ser	Thr	Gly	Val	Val	Ser	Glu	Pro	Phe	Thr	Leu	Asn	Phe	
			180				185					190			
Thr	Ile	Asn	Asn	Leu	Arg	Tyr	Met	Ala	Asp	Met	Gly	Gln	Pro	Gly	Ser
	195					200					205				
Leu	Lys	Phe	Asn	Ile	Thr	Asp	Asn	Val	Met	Lys	His	Leu	Leu	Ser	Pro

210		215		220
Leu Phe Gln Arg Ser	Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val			
225	230	235	240	
Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu				
	245	250	255	
Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys				
	260	265	270	
Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu				
	275	280	285	
Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn				
	290	295	300	
Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr				
305	310	315	320	
Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu				
	325	330	335	
Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro				
	340	345	350	
Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu				
	355	360	365	
Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe				
	370	375	380	
Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala				
385	390	395	400	
Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly				
	405	410	415	
Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr				
	420	425	430	
His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu				
	435	440	445	
Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr				
	450	455	460	
Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro				
465	470	475	480	
Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val				
	485	490	495	
Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys				
	500	505	510	
Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys Ala				
	515	520	525	
Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu				
	530	535	540	
Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln				
545	550	555	560	
Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro				
	565	570	575	
Thr Ser Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr				
	580	585	590	
Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr				
	595	600	605	
Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg				
	610	615	620	
Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe				
625	630	635	640	
Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn				
	645	650	655	
Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu				
	660	665	670	
Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu				
	675	680	685	
Asp Arg Ser Ser Val Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu				
690	695	700		

Pro Leu Thr Gly Asn Ser Ala Asp Ile Gln His Ser Gly Gly Arg Ser
705 710 715 720
Ser Leu Glu Gly Pro Arg Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp
725 730 735
Leu Asn Met His Thr Gly His His His His His His
740 745

<210> 2
<211> 809
<212> PRT
<213> Artificial Sequence

<220>
<223> CA 125/0772P 3-repeat TM

<400> 2
Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr Lys Leu Phe Thr His
1 5 10 15
Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr
20 25 30
Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala
35 40 45
Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
50 55 60
Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr
65 70 75 80
Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
85 90 95
Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
100 105 110
Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro
115 120 125
Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu
130 135 140
Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
145 150 155 160
Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
165 170 175
Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe
180 185 190
Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser
195 200 205
Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro
210 215 220
Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val
225 230 235 240
Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu
245 250 255
Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys
260 265 270
Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu
275 280 285
Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn
290 295 300
Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr
305 310 315 320
Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu
325 330 335
Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro

<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VH1 CDR

<400> 3
Gly Phe Ser Leu Ser Thr Pro Gly Met Gly Val Gly
1 5 10

<210> 4
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VH2 CDR

<400> 4
His Ile Trp Trp Asp Asp Phe Lys Arg Asp Asn Pro Ala Leu Lys Ser
1 5 10 15

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VH3 CDR

<400> 5
Val Asp Gly Asn Phe Leu Ser Trp Tyr Phe Asp Val
1 5 10

<210> 6
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VL1 CDR

<400> 6
Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 117.1 VL2 CDR

<400> 7
Lys Val Ser Asn Arg Phe Ser

1 5

 <210> 8
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> 117.1 VL3 CDR

 <400> 8
 Ser Gln Ser Arg Tyr Val Pro Glu Thr
 1 5

 <210> 9
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> 368.1 VH1 CDR

 <400> 9
 Gly Tyr Ser Phe Thr Gly Phe Tyr Met His
 1 5 10

 <210> 10
 <211> 17
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> 368.1 VH2 CDR

 <400> 10
 Tyr Val Ser Cys Tyr Thr Gly Ala Thr Thr Tyr Thr Gln Lys Phe Lys
 1 5 10 15
 Gly

 <210> 11
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> 368.1 VH3 CDR

 <400> 11
 Glu Gly Asp Tyr Tyr Ser Met Asp Phe
 1 5

 <210> 12
 <211> 16
 <212> PRT

<213> Artificial Sequence

<220>

<223> 368.1 VL1 CDR

<400> 12

Arg	Ser	Ser	Gln	Ser	Leu	Glu	Arg	Thr	Asn	Gly	Asn	Thr	Tyr	Leu	His
1				5					10					15	

<210> 13

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 368.1 VL2 CDR

<400> 13

Lys	Val	Ser	Ser	Arg	Phe	Ser
1				5		

<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 368.1 VL3 CDR

<400> 14

Ser	Gln	Thr	Thr	His	Gly	Pro	Pro	Thr
1				5				

<210> 15

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 501.1 VH1 CDR

<400> 15

Gly	Tyr	Ile	Phe	Thr	Asp	Tyr	Gly	Met	Asn
1				5					10

<210> 16

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 501.1 VH2 CDR

<400> 16

Cys	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Thr	Ile	Tyr	Ser	Asp	Asp	Phe	Arg
1				5					10					15	

Gly

<210> 17
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 VH3 CDR

<400> 17
Gly Asn Tyr Arg Asp Ala Ile Asp Tyr
1 5

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 VL1 CDR

<400> 18
Lys Ala Ser Gln Asp Ile Lys Ser Tyr Leu Ser
1 5 10

<210> 19
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 VL2 CDR

<400> 19
Tyr Ala Thr Thr Leu Ala Asp
1 5

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 VL3 CDR

<400> 20
Leu His His Asp Glu Ser Pro Phe Thr
1 5

<210> 21
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> 776.1 VH1 CDR

<400> 21

Gly Tyr Thr Phe Thr Asp Tyr Asn Ile His
1 5 10

<210> 22

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> 776.1 VH2 CDR

<400> 22

Tyr Ile Tyr Pro Tyr Asn Gly Val Ser Asp Tyr Asn Gln Asn Phe
1 5 10 15

<210> 23

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> 776.1 VH3 CDR

<400> 23

Arg Trp Asp Phe Gly Ser Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 24

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 776.1 VL1 CDR

<400> 24

Arg Ala Ser Ser Ser Val Ile Tyr Met Cys
1 5 10

<210> 25

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 776.1 VL2 CDR

<400> 25

Gly Thr Ser Thr Leu Ala Ser
1 5

<210> 26

<211> 9

<212> PRT
 <213> Artificial Sequence

<220>
 <223> 776.1 VL3 CDR

<400> 26
 Gln Gln Trp Ser Ser Asn Pro Phe Thr
 1 5

<210> 27
 <211> 131
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 117.1 light chain polypeptide variable region (117.1L)

<400> 27
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
 1 5 10 15
 Ser Ser Ser Asp Ala Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
 20 25 30
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
 35 40 45
 Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
 50 55 60
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
 65 70 75 80
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95
 Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
 100 105 110
 Ser Gln Ser Arg Tyr Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125
 Glu Ile Lys
 130

<210> 28
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 117.1 heavy chain polypeptide variable region (117.1H)

<400> 28
 Met Gly Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
 1 5 10 15
 Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 20 25 30
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 35 40 45
 Ser Thr Pro Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
 50 55 60
 Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Phe Lys Arg Asp
 65 70 75 80
 Asn Pro Ala Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser

				85						90					95				
Ser	Gln	Val	Phe	Leu	Lys	Ile	Ala	Ser	Val	Asp	Thr	Ala	Asp	Thr	Ala				
			100					105					110						
Thr	Tyr	Tyr	Cys	Val	Arg	Val	Asp	Gly	Asn	Phe	Leu	Ser	Trp	Tyr	Phe				
		115					120					125							
Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser							
	130					135					140								

<210> 29
 <211> 131
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 368.1 light chain polypeptide variable region (368.1L)

Met	Lys	Leu	Pro	Val	Arg	Leu	Leu	Val	Leu	Met	Phe	Trp	Ile	Pro	Ala				
1				5					10					15					
Ser	Ser	Ser	Asp	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val				
			20					25					30						
Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu				
		35				40					45								
Glu	Arg	Thr	Asn	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro				
	50				55						60								
Gly	Gln	Ser	Pro	Lys	Leu	Ile	Tyr	Lys	Val	Ser	Ser	Arg	Phe	Ser					
65				70				75					80						
Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr				
				85				90					95						
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Ile	Tyr	Phe	Cys				
			100					105					110						
Ser	Gln	Thr	Thr	His	Gly	Pro	Pro	Thr	Cys	Gly	Gly	Gly	Thr	Lys	Leu				
	115					120						125							
Glu	Ile	Lys																	
	130																		

<210> 30
 <211> 137
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 368.1 heavy chain polypeptide variable region (368.1H)

Met	Gly	Trp	Ile	Trp	Ile	Phe	Leu	Phe	Leu	Leu	Ser	Gly	Thr	Ala	Gly				
1				5					10					15					
Val	His	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Arg				
			20					25					30						
Thr	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe				
		35				40						45							
Thr	Gly	Phe	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	Leu	Gly	Lys	Ser	Leu				
	50				55						60								
Glu	Trp	Ile	Gly	Tyr	Val	Ser	Cys	Tyr	Thr	Gly	Ala	Thr	Thr	Tyr	Thr				
65				70				75						80					

Gln Lys Phe Lys Gly Lys Ala Thr Phe Thr Val Asp Thr Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Glu Gly Asp Tyr Tyr Ser Met Asp Phe Trp Gly
115 120 125

Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

<210> 31
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 light chain polypeptide variable region (501.1L)

<400> 31
Met Asp Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp
1 5 10 15

Phe Pro Gly Ile Arg Cys Asp Ile Lys Met Thr Gln Ser Pro Ser Ser
20 25 30

Ile Tyr Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45

Gln Asp Ile Lys Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys
50 55 60

Ser Pro Lys Thr Leu Ile Tyr Tyr Ala Thr Thr Leu Ala Asp Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Ile
85 90 95

Ile Asn Ser Leu Glu Ser Asp Asp Ile Ala Thr Tyr Phe Cys Leu His
100 105 110

His Asp Glu Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125

<210> 32
<211> 137
<212> PRT
<213> Artificial Sequence

<220>
<223> 501.1 heavy chain polypeptide variable region (501.1H)

<400> 32
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30

Pro Gly Glu Thr Val Gln Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe
35 40 45

Thr Asp Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
50 55 60

Lys Trp Met Gly Cys Ile Asn Thr Tyr Thr Gly Glu Thr Ile Tyr Ser
65 70 75 80

Asp Asp Phe Arg Gly Arg Phe Ala Ile Ser Leu Glu Thr Ser Ala Ser
85 90 95

Thr Ala Phe Ile Gln Ile Asn Asn Leu Lys Asn Glu Asp Ala Ala Thr
100 105 110

Tyr Phe Cys Ala Arg Gly Asn Tyr Arg Asp Ala Ile Asp Tyr Trp Gly
115 120 125
Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

<210> 33
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 light chain polypeptide variable region (776.1L)

<400> 33
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Phe Ala Ser Pro Gly Glu Thr Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ile Tyr Met Cys Trp Asn Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Gly Thr Ser Thr Leu Ala Ser Gly Val Pro
65 70 75 80
Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
115 120 125

<210> 34
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> 776.1 heavy chain polypeptide variable region (776.1H)

<400> 34
Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser His Gly Lys Ile Leu
50 55 60
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Val Ser Asp Tyr Asn
65 70 75 80
Gln Asn Phe Lys Ser Lys Ala Thr Leu Ile Val Asp Asn Ser Ser Asn
85 90 95
Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Asp Phe Gly Ser Gly Tyr Tyr Phe Asp Tyr
115 120 125
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
130 135

<210> 35
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> 117.1 light chain polypeptide variable region (117.1L)

<400> 35
atgaagttgc ctggttaggct gttggtgctg atgttctgga ttcttggttc cagcagtgat 60
gctgtgatga cccaaactcc actctccctg cctgtcagtc ttggagatca ggcctccatc 120
tcttgcatga ctagtcagag ccttgtagac agtaatggaa acacctattt acattggtac 180
ctgcagaagc caggccagtc tccaaaactc ctgatctaca aagtttccaa ccgattttct 240
ggggtccag acaggttcag tggcagtggg tcagggacag atttcacact caggatcagc 300
agagtggagg ctgaggatct gggagtttat ttctgctctc aaagtagata tggtccgtgg 360
acgttcggtg gaggcaccaa gctggaaatc aaa 393

<210> 36
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> 117.1 heavy chain polypeptide variable region (117.1H)

<400> 36
atgggcaggc ttactttctc attcctgcta ctgattgtcc ctgcatatgt cctgtcccag 60
gttactctga aagagtctgg ccctgggata ttgcagccct cccagaccct cagtctgact 120
tggtctttct ctgggttttc actgagcact cctggtagtg gtgtaggctg gattcgtag 180
ccatcagggg agggctctgga gtggctggca cacatttggg gggatgattt caagcgcat 240
aatccagccc ttaagagccg actgactatc tctaaggata cctccagcag ccagggttttc 300
ctcaaatcgc ccagtgtgga cactgcagat actgccacat attactgtgt tcgagtggat 360
ggtaacttcc tctcctggta ttctgatgtc tggggcgctg ggaccacggt caccgtctcc 420
tca 423

<210> 37
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> 368.1 light chain polypeptide variable region (368.1L)

<400> 37
atgaagttgc ctggttaggct gttggtgctg atgttctgga ttcttgcttc cagcagtgat 60
gttgtgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc 120
tcttgcatga ctagtcagag ccttgaacgc actaatggaa acacctattt acattggtac 180
ctgcagaagc caggccagtc tccaaaactc ctgatctaca aagtttccag ccgattttct 240
ggggtccag ataggttcag tggcagtggg tcagggacag atttcacact caagatcagt 300
agagtggagg ctgaggatct ggggaatttat ttctgttctc aaactacaca tggctcctccg 360
acgtgcggtg gaggcaccaa gctggaaatc aaa 393

<210> 38
<211> 411
<212> DNA

<213> Artificial Sequence

<220>

<223> 368.1 heavy chain polypeptide variable region (368.1H)

<400> 38

```
atgggatgga tctggatctt tctcttcctc ctgtcaggaa ctgcagggtg ccactctgag 60
gtccagctgc agcagtctgg acctgagtta gtgaggactg gggcttcagt gaagatatcc 120
tgcaaggctt ctgggttactc attcactggg ttctacatgc actgggtcaa gcagagcctt 180
ggaaagagcc ttgagtggat tggatatgtt agttgttaca ctgggtgctac tacctacacc 240
cagaagttca agggcaaggc cacatttact gttgacacat cctccagcac agcctacatg 300
caactcaaca gcctgacatc tgaagactct gcggtctatt actgtgcaag agaaggggat 360
tactattcta tggactttctg gggcaagga acctcagtca ccgtctcctc a 411
```

<210> 39

<211> 386

<212> DNA

<213> Artificial Sequence

<220>

<223> 501.1 light chain polypeptide variable region (501.1L)

<400> 39

```
atggacatga gggcccctgc tcagtttttt gggatcttgt tgctctgggt tccaggtatc 60
agatgtgaca tcaagatgac ccagtctcca tcgtccattt atgcatcgct gggagagagg 120
gtcactataa cttgcaaggc gagtccaggc attaaaagct atttaagctg gtaccaacag 180
aaaccctgga aatctcctaa gaccctgac tattatgcaa caaccttggc agatgggggtc 240
ccatcaagat tcagtggcag tggatctggg caagattatt ctctaatacat caacagcctg 300
gagtctgacg atatatgctac ttatttctgt ctacaccatg atgagagccc attcacgttc 360
ggctcgggga caaaattgga aataaa 386
```

<210> 40

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> 501.1 heavy chain polypeptide variable region (501.1H)

<400> 40

```
atggcttggt tgtggacctt gctgttcctg atggcagctg cccaaagtgc ccaagcacag 60
atccagttgg tgcagtctgg acctgagctg aagaagcctg gagagacagt ccagatctcc 120
tgcaaggctt ctggctatat cttcacagac tatggaatga actgggtgaa acaggctcca 180
ggaaagggtt taaaatggat gggctgtata aacacctaca ctggagagac aatatatagt 240
gatgacttca ggggacgggt tgccatctct ttggaaacct ctgccagcac tgcctttatt 300
cagatcaaca acctcaaaaa tgaggacgcg gcaacatatt tctgtgcaag gggaaattac 360
agggatgcta ttgactattg gggcaagga acctcagtca ccgtctcctc a 411
```

<210> 41

<211> 383

<212> DNA

<213> Artificial Sequence

<220>

<223> 776.1 light chain polypeptide variable region (776.1L)

<400> 41

```
atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60
agaggacaaa ttgttctctc ccagtctcca gcaatcctgt ttgcatctcc aggggagacg 120
gtcacaatga cttgcagggc cagttcaagt gtaatttaca tgtgttgga tccagcagaag 180
```

```

ccaggatcct cccccaacc ctggatttat ggcacatcca ccttggttc tggagtcct 240
actcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagagtagag 300
gctgaagatg ctgccactta ttactgccag cagtggagta gtaacccatt cacgttcggc 360
tcggggacaa agttggaaat aaa 383

```

```

<210> 42
<211> 417
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> 776.1 heavy chain polypeptide variable region (776.1H)

```

```

<400> 42
atgggatgga gctggatctt tctcttcctc ctgtcaggaa ctgcaggcgt ccactctgag 60
gtccagcttc agcagtcagg acctgagctg gtgaaacctg gggcctcagt gaagatatcc 120
tgcaaggctt ctggatacac attcactgac tacaacattc actgggtgaa acagagccat 180
ggaaagatcc ttgagtggat tggatatatt tatccttata atggtgtttc tgactacaac 240
cagaatttca agagcaaggc cacattgatt gtagacaatt cctccaacac agcctacatg 300
gaactccgca gcctgacatc tgaggactct gcagtctatt attgtgcaag atgggacttc 360
ggtagtggct actactttga ctactggggc caaggcacca ctctcacagt ctctca 417

```

```

<210> 43
<211> 45
<212> RNA
<213> Artificial Sequence

```

```

<220>
<223> primer (see section 6.6)

```

```

<400> 43
rcgacuggag cacgaggaca cugacaugga cugaaggagu agaaa 45

```

```

<210> 44
<211> 54
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> primer (see section 6.6)

```

```

<400> 44
gctgtcaacg atacgctacg taacggcatg acagtgtttt tttttttttt tttt 54

```

```

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> primer (see section 6.6)

```

```

<400> 45
ayctccacac acaggrrcca gtggatagac 30

```

```

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

```


<220>
 <223> primer (see section 6.6)

<400> 46
 ggatacagtt ggtgcagcat c 21

<210> 47
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer (see section 6.6)

<400> 47
 cgactggagc acgaggacac tga 23

<210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer (see section 6.6)

<400> 48
 attaaccctc actaaaggga 20

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer (see section 6.6)

<400> 49
 taatacgact cactataggg 20

<210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer (see section 6.6)

<400> 50
 attaaccctc actaaaggga 20

<210> 51
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer (see section 6.6)

<400> 51
 taatacgact cactataggg 20

<210> 52
 <211> 383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 725.1 light chain polypeptide variable region (725.1L)

<400> 52
 atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataatgtcc 60
 agaggacaaa ttattctctc ccagtctcca gcaatcctgt ctgcatctcc aggggagaag 120
 gtcacaatga cttgcagggc cagttcaagt gtaagttcca ttcactggta ccagcagaag 180
 ccagaatcct cccccaacc ctggatttac gccacatcca acctggcttc tggagtcct 240
 gttcgcttca gtggcagtggt gtctgggacc tcttatactc tcacaatcag cagaatggag 300
 gctgcagatg ctgccactta ttactgccag cagtggagta ttgatccagc cacgttcgga 360
 ggggggacca agctggaaat aaa 383

<210> 53
 <211> 135
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 725.1 heavy chain polypeptide variable region (725.1H)

<400> 53
 Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 1 5 10 15
 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30
 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 35 40 45
 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Lys Trp Met Gly Trp Ile Asn Ala Tyr Ile Gly Glu Pro Thr Tyr Ala
 65 70 75 80
 Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Ala Ser Thr His
 85 90 95
 Thr Ala Tyr Leu Gln Ile Asn Ser Leu Lys Ser Glu Asp Thr Ala Thr
 100 105 110
 Tyr Phe Cys Ala Ser Gly Gly Asn Ser Leu Asp Phe Trp Gly Gln Gly
 115 120 125
 Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 54
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 725.1 light chain polypeptide variable region (725.1L)

<400> 54
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Gln Ile Ile Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Ser	Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Glu	Ser	Ser
	50					55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65					70					75					80
Val	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Thr	Leu	Thr	Ile
				85					90					95	
Ser	Arg	Met	Glu	Ala	Ala	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Ile	Asp	Pro	Ala	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	
		115					120					125			

<210> 55
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 16H9 heavy chain polypeptide variable region (16H9H)

Met	Lys	Cys	Ser	Trp	Val	Ile	Phe	Phe	Leu	Met	Ala	Val	Val	Thr	Gly
1				5					10					15	
Val	Asn	Ser	Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys
			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile
		35					40					45			
Lys	Asp	Thr	Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Arg	Ile	Asp	Pro	Ala	Asn	Gly	Asn	Thr	Lys	Tyr	Asp
65					70				75						80
Pro	Lys	Phe	Gln	Gly	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn
				85					90					95	
Thr	Ala	Tyr	Val	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		
Tyr	Tyr	Cys	Ala	Ser	Ser	Asp	Ile	Tyr	Tyr	Gly	Asn	Pro	Gly	Gly	Phe
		115					120				125				
Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala			
		130					135					140			

<210> 56
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 16H9 light chain polypeptide variable region (16H9L)

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Met	Ser	Ala	Ser	Leu	Gly	Glu	Arg	Val	Thr	Met	Thr	Cys	Thr	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Ser	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly
	50						55					60			

Ser	Ser	Pro	Lys	Leu	Trp	Ile	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly
65					70					75					80
Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu
				85						90				95	
Thr	Ile	Ser	Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His
			100					105					110		
Gln	Tyr	His	Arg	Ser	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu
		115					120					125			
Ile															

<210> 57
 <211> 406
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 725.1 heavy chain polypeptide variable region (725.1H)

<400> 57
 atggccttggg tgtggacctt gctattcctg atggcagctg cccaaagtgc ccaagcacag 60
 atccagttgg tgcagtctgg acctgaactg aagaagcctg gagagacagt caagatctcc 120
 tgcaaggctt ctggatattc cttcacaaac tatggaatga actgggtgaa gcaggctcca 180
 gggaagggtt taaagtggat gggctggata aacgcctaca ttggagagcc aacatatgct 240
 gatgacttca agggacgatt tgccttctct ctggaagcct ctaccacac tgcctatttg 300
 cagatcaaca gcctcaaaag tgaggacacg gctacatatt tctgtgcaag tgggggtaac 360
 tcccttgact tttggggcca aggcaccact ctcacagtct cctcag 406

<210> 58
 <211> 423
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 16H9 heavy chain polypeptide variable region (16H9H)

<400> 58
 atgaaatgca gctgggttat cttcttctctg atggcagctg ttacaggggt caattcagag 60
 gttcagctgc agcagtctgg ggcagagctt gtgaagccag gggcctcagt caagtgtcc 120
 tgcacagctt ctggcttcaa cattaaagac acctatatgc actgggtgaa gcagaggcct 180
 gaacagggcc tggagtggat tggaaggatt gatcctgcga atggtaatac taaatatgac 240
 ccgaagttcc agggcaaggc cactataaca gcagacacat cctccaacac agcctacgtg 300
 cagctcagca gcctgacatc tgaggacact gccgtctatt actgtgctag tagtgacatc 360
 tactatggta accccggggg gtttgcttac tggggccaag ggactctggt cactgtctct 420
 gca 423

<210> 59
 <211> 389
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 16H9 light chain polypeptide variable region (16H9L)

<400> 59
 atggattttc aggtgcagat ttccagcttc ctgctaataca gtgcctcagt cataatgtcc 60
 agaggacaaa ttgttctcac ccagtctcca gcaatcatgt ctgcatctct aggggaacgg 120
 gtcaccatga cctgcactgc cagctcaagt gtaagtcca gttacttgca ctgggtaccag 180
 cagaagccag gatcctcccc caaactctgg atttatagca catccaacct ggcttctgga 240
 gtcccagctc gcttcagtgg cagtgggtct gggacctctt actctctcac aatcagcagc 300

atggaggctg aagatgctgc cacttattac tgccaccagt atcatcggtc cccattcacg 360
 ttcggctcgg ggacaaagtt ggaaataaaa 389

<210> 60
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 725.1 VH1 CDR

<400> 60
 Gly Tyr Ser Phe Thr Asn Tyr Gly Met Asn
 1 5 10

<210> 61
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 725.1 VH2 CDR

<400> 61
 Trp Ile Asn Ala Tyr Ile Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
 1 5 10 15
 Gly

<210> 62
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 725.1 VH3 CDR

<400> 62
 Gly Gly Asn Ser Leu Asp Phe
 1 5

<210> 63
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 725.1 VL1 CDR

<400> 63
 Arg Ala Ser Ser Ser Val Ser Ser Ile His
 1 5 10

<210> 64
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 725.1 VL2 CDR

<400> 64

Ala Thr Ser Asn Leu Ala Ser

1 5

<210> 65

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> 725.1 VL3 CDR

<400> 65

Gln Gln Trp Ser Ile Asp Pro Ala Thr

1 5

<210> 66

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 16H9 VH1 CDR

<400> 66

Gly Phe Asn Ile Lys Asp Thr Tyr Met His

1 5 10

<210> 67

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 16H9 VH2 CDR

<400> 67

Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln

1 5 10 15

Gly

<210> 68

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 16H9 VH3 CDR

<400> 68

Ser Asp Ile Tyr Tyr Gly Asn Pro Gly Gly Phe Ala Tyr

1	5	10
---	---	----

<210> 69
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 16H9 VL1 CDR

<400> 69
 Thr Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
 1 5 10

<210> 70
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 16H9 VL2 CDR

<400> 70
 Ser Thr Ser Asn Leu Ala Ser
 1 5

<210> 71
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 16H9 VL3 CDR

<400> 71
 His Gln Tyr His Arg Ser Pro Phe Thr
 1 5